

J.
Roark

16
gnd



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,955A

DATE: 10/02/2002

TIME: 14:38:38

Input Set : A:\78104023.ST25.txt

Output Set: N:\CRF4\10022002\I806955A.raw

3 <110> APPLICANT: Gabriel, Panayi S
4 Corrigall, Valerie
5 Bodman-Smith, Mark
6 Fife, Mark
7 Lanchbury, Jeremy
9 <120> TITLE OF INVENTION: Treatment of Inflammatory Disease
11 <130> FILE REFERENCE: 78104.023/N10984
13 <140> CURRENT APPLICATION NUMBER: 09/806,955A
14 <141> CURRENT FILING DATE: 2001-07-11
16 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03316
17 <151> PRIOR FILING DATE: 1999-10-08
19 <150> PRIOR APPLICATION NUMBER: 9822115.3
20 <151> PRIOR FILING DATE: 1999-10-09
22 <160> NUMBER OF SEQ ID NOS: 9
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 639
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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42 35 40 45
45 Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
46 50 55 60
49 Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
50 65 70 75 80
53 Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
54 85 90 95
57 Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
58 100 105 110
61 Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
62 115 120 125
65 Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
66 130 135 140
69 Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
70 145 150 155 160
73 Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
74 165 170 175
77 Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly

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81 Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
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85 Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe
86          210          215          220
89 Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
90 225          230          235          240
93 Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
94          245          250          255
97 Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
98          260          265          270
101 Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
102          275          280          285
105 Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
106          290          295          300
109 Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
110 305          310          315          320
113 Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
114          325          330          335
117 Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
118          340          345          350
121 Ile Gln Gln Leu Val Lys Glu Phe Asn Gly Lys Glu Pro Ser Arg
122          355          360          365
125 Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
126          370          375          380
129 Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
130 385          390          395          400
133 Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
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137 Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
138          420          425          430
141 Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
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145 Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
146          450          455          460
149 Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
150 465          470          475          480
153 Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
154          485          490          495
157 Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
158          500          505          510
161 Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
162          515          520          525
165 Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
166          530          535          540
169 Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
170 545          550          555          560
173 Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
174          565          570          575

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177 Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
178          580          585          590
181 Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
182          595          600          605
185 Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro Pro Pro
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193 <210> SEQ ID NO: 2
194 <211> LENGTH: 633
195 <212> TYPE: PRT
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208 Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser Tyr Val
209          35          40          45
212 Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
213          50          55          60
216 Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
217 65          70          75          80
220 Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
221          85          90          95
224 Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
225          100         105         110
228 Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
229          115         120         125
232 Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
233          130         135         140
236 Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
237 145         150         155         160
240 Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
241          165         170         175
244 Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
245          180         185         190
248 Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
249          195         200         205
252 Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe
253          210         215         220
256 Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
257 225         230         235         240
260 Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
261          245         250         255
264 Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
265          260         265         270
268 Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
269          275         280         285

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273      290                      295                      300
276 Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
277 305                      310                      315                      320
280 Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
281                      325                      330                      335
284 Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
285                      340                      345                      350
288 Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg
289                      355                      360                      365
292 Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
293      370                      375                      380
296 Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
297 385                      390                      395                      400
300 Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
301                      405                      410                      415
304 Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
305                      420                      425                      430
308 Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
309                      435                      440                      445
312 Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
313      450                      455                      460
316 Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
317 465                      470                      475                      480
320 Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
321                      485                      490                      495
324 Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
325                      500                      505                      510
328 Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
329                      515                      520                      525
332 Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
333      530                      535                      540
336 Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
337 545                      550                      555                      560
340 Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
341                      565                      570                      575
344 Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
345                      580                      585                      590
348 Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
349                      595                      600                      605
352 Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro Pro Pro
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357 625                      630
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361 <211> LENGTH: 1917
362 <212> TYPE: DNA
363 <213> ORGANISM: Homo sapiens
365 <400> SEQUENCE: 3

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370 aaccgcatca cgcgctccta tgtcgcttcc actcctgaag gggaaactgt gattggcgat 180
372 gccgccaaga accagctcac ctccaacccc gagaacacgg tctttgacgc caagcggctc 240
374 atcggccgca cgtggaatga cccgtctgtg cagcaggaca tcaagttctt gccgttcaag 300
376 gtggttgaaa agaaaactaa accatacatt caagttgata ttggagggtg gcaaacaaag 360
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418 gaaaggatgg ttaatgatgc tgagaagttt gctgaggaag acaaaaagct caaggagcgc 1620
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426 aagaagaagg aactggaaga aattgttcaa ccaattatca gcaaactcta tggaaagtga 1860
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434 <213> ORGANISM: Artificial sequence
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437 <223> OTHER INFORMATION: Primer
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449 <223> OTHER INFORMATION: Primer
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VERIFICATION SUMMARY

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